

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:01:42 ; Search time 55 Seconds
(without alignments)
30.823 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      1586107 segs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- ```

1: A_Geneseq_29Jan04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match Length | DB | ID | Description |
|------------|-------|--------------------|----|----|-------------|
| 1          | 40    | 100.0              | 6  | 5  | AA#48538    |
| 2          | 40    | 100.0              | 6  | 5  | AA#48570    |
| 3          | 40    | 100.0              | 6  | 6  | AD#61814    |
| 4          | 40    | 100.0              | 6  | 6  | AD#61846    |
| 5          | 40    | 100.0              | 7  | 5  | AA#48574    |
| 6          | 40    | 100.0              | 7  | 6  | AD#61850    |
| 7          | 40    | 100.0              | 8  | 5  | AA#48575    |
| 8          | 40    | 100.0              | 8  | 5  | AA#48567    |
| 9          | 40    | 100.0              | 8  | 6  | AD#61851    |
| 10         | 40    | 100.0              | 8  | 6  | AD#61843    |
| 11         | 40    | 100.0              | 9  | 5  | AA#48573    |
| 12         | 40    | 100.0              | 9  | 5  | AA#48566    |
| 13         | 40    | 100.0              | 9  | 5  | AA#48569    |
| 14         | 40    | 100.0              | 9  | 5  | AA#48572    |
| 15         | 40    | 100.0              | 9  | 6  | AD#61848    |
| 16         | 40    | 100.0              | 9  | 6  | AD#61841    |
| 17         | 40    | 100.0              | 9  | 6  | AD#61849    |
| 18         | 40    | 100.0              | 9  | 6  | AD#61845    |
| 19         | 40    | 100.0              | 9  | 6  | AD#61842    |
| 20         | 40    | 100.0              | 10 | 5  | AA#48568    |
| 21         | 40    | 100.0              | 10 | 5  | AA#48571    |
| 22         | 40    | 100.0              | 10 | 6  | AD#61844    |
| 23         | 40    | 100.0              | 10 | 6  | AD#61847    |
| 24         | 40    | 100.0              | 11 | 5  | AA#48565    |
| 25         | 40    | 100.0              | 11 | 6  | AD#61840    |

|    |    |      |     |   |          |           |             |
|----|----|------|-----|---|----------|-----------|-------------|
| 26 | 37 | 92.5 | 133 | 4 | AAU21305 | Aau21305  | Human nov   |
| 27 | 37 | 92.5 | 103 | 2 | AAU06332 | Aay06332  | Gliocloadi  |
| 28 | 37 | 92.5 | 236 | 2 | AAU06363 | Aay06363  | Gliocloadi  |
| 29 | 37 | 92.5 | 236 | 3 | AAH48341 | Aay84341  | Amino aci   |
| 30 | 37 | 92.5 | 236 | 3 | AAH14876 | Aab14876  | Gliocloadi  |
| 31 | 37 | 92.5 | 236 | 5 | AAU77584 | Aau77584  | G. roseum   |
| 32 | 37 | 92.5 | 236 | 5 | AAU77428 | Aau77428  | Gliocloadi  |
| 33 | 37 | 92.5 | 274 | 5 | ABP65718 | Abp65718  | B.f.fibobac |
| 34 | 37 | 92.5 | 597 | 4 | ABB62635 | Abb62635  | Drosophill  |
| 35 | 37 | 92.5 | 885 | 4 | AAU33594 | Aabb3594  | Pseudomon   |
| 36 | 37 | 92.5 | 885 | 6 | ABU15648 | Abou15648 | Protein e   |
| 37 | 36 | 90.0 | 6   | 5 | ABB08727 | Abb08727  | Mutated I   |
| 38 | 36 | 90.0 | 6   | 5 | ABB08728 | Abb08728  | Mutated I   |
| 39 | 36 | 90.0 | 6   | 5 | AAH48537 | Aam48537  | Anti- infel |
| 40 | 36 | 90.0 | 6   | 5 | AAH48548 | Aam48548  | Anti- infel |
| 41 | 36 | 90.0 | 6   | 5 | AAH48559 | Aam48559  | Anti- infel |
| 42 | 36 | 90.0 | 6   | 5 | AAH48509 | Aam48509  | NBD mutan   |
| 43 | 36 | 90.0 | 6   | 5 | AAH48510 | Aam48510  | NBD mutan   |
| 44 | 36 | 90.0 | 6   | 5 | AAH48536 | Aam48536  | Anti- infel |
| 45 | 36 | 90.0 | 6   | 6 | ABU08420 | Abu08420  | Human NEM   |

## ALIGNMENTS

|          |                                  |
|----------|----------------------------------|
| RESULT 1 |                                  |
| AAM48538 |                                  |
| ID       | AAM48538 standard; peptide; 6 AA |

AC AAM48538;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 41.

Ant

KW  
imncyt  
KW

KW aut

KW ata

OS  
Syst

PN W0200183554-A2

PD 08-NOV-2001

02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

PA (UYYA ) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

DR WPI; 2002-121889/16.

Nov  
PT  
DT

act

PS  
xy

CC The

CC AMM  
CC rps

The invention relates to an antiinflammatory compound (especially, AA848620-AA848655), comprising a membrane translocation domain (AA848620-AA848657 or AA848646-AA848651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AA848525-AA848619). The

CC antiinflammatory compounds have antiasthmatic, cytosstatic, antipsoriatic,  
 CC antineumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, virocidic and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

CC Sequence 6 AA;

Query Match 100.0%; Score 40; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Gaps 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 1 ADMSWA 6

RESULT 2  
 AAM48570 standard; peptide; 6 AA.

AC AAM48570;

DE 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 73.

KM Antinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;  
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KM immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX MO200183554-A2.

PN 08-NOV-2001.

PD 02-MAY-2001; 2001MO-US014346.

PF 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA ) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K,

DR WPI, 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

XX activation, and for treating asthma, lung inflammation, psoriasis.

CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC antiinflammatory compounds have antiasthmatic, cytosstatic, antipsoriatic,  
 CC antineumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, virocidic and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

CC Sequence 6 AA;

Query Match 100.0%; Score 40; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Gaps 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 1 ADMSWA 6

RESULT 3  
 ADA61814 standard; peptide; 6 AA.

AC ADA61814;

DE 20-NOV-2003 (first entry).

XX NF-kB essential modulator (NEMO) binding peptide #14.

KM NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
 KM antiinflammatory; antiasthmatic; antipsoriatic; antineumatic;  
 KM antithrombotic; osteopathic; antibacterial; immunosuppressive;  
 KM dermatological; neuroprotective; cytosstatic; nootropic; virocidic;  
 KM gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 KM psoriasis; rheumatoid arthritis; osteoarthritis;  
 KM inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
 KM systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 KM Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 KM necrosis factor kappa B essential modulator.

OS Unidentified.

XX US2003054999-A1.

PN 20-MAR-2003.

PD 02-MAY-2001; 2001US-00847946.

PF 02-MAY-2000; 2000US-0201261P.

PR 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PI (FINN/) FINDEIS M A.

DR (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G,

PI WPI, 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
 PT cancer, comprises a membrane translocation domain and a NEMO binding  
 PT sequence.  
 XX  
 PS Claim 6; Page 23; 37pp; English.  
 CC  
 CC The invention describes an anti-inflammatory compound comprising (1). The  
 CC compound is useful for diagnosing or treating inflammatory disorders,  
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.,  
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
 CC Alzheimer's disease or viral infection. This is the amino acid sequence  
 CC of an anti-inflammatory peptide that binds to, and down-regulates,  
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
 CC  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 DB 1 ADMSWA 6  
 RESULT 4  
 ADA61846  
 ID ADA61846 standard; peptide; 6 AA.  
 XX  
 AC ADA61846;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE NFkB essential modulator (NEMO) binding peptide #46.  
 XX  
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
 KW anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
 KW dermatologic; neuroprotective; cytostatic; nootropic; virucide;  
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 KW psoriasis; rheumatoid arthritis; osteoarthritis;  
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 KW necrosis factor kappa B essential modulator.  
 KW  
 XX  
 OS Unidentified.  
 XX  
 PN US2003054999-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 02-MAY-2001; 2001US-00847946.  
 XX  
 PR 02-MAY-2000; 2000US-0201261P.  
 XX  
 PA (MAYN/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 PA (FIND/) FINDELS M. A.  
 PA (PHIL/) PHILLIPS K.  
 PA (HANN/) HANNIG G.  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K, Hannig G;  
 XX  
 DR MPI; 2003-596541/56.  
 XX  
 PT New compound for diagnosing or treating inflammatory disorders, e.g.  
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
 PT cancer, comprises a membrane translocation domain and a NEMO binding  
 PT sequence.

XX  
 PS Claim 6; Page 23; 37pp; English.  
 CC  
 CC The invention describes an anti-inflammatory compound comprising (1). The  
 CC compound is useful for diagnosing or treating inflammatory disorders,  
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.,  
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
 CC Alzheimer's disease or viral infection. This is the amino acid sequence  
 CC of an anti-inflammatory peptide that binds to, and down-regulates,  
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
 CC  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 DB 1 ADMSWA 6  
 RESULT 5  
 AAM48574  
 ID AAM48574 standard; peptide; 7 AA.  
 XX  
 AC AAM48574;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 77.  
 XX  
 XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NK-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW autoimmunity; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014346.  
 XX  
 PR 02-MAY-2000; 2000US-0201261P.  
 XX  
 PR 22-AUG-2000; 2000US-00643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K;  
 XX  
 DR MPI; 2002-121889/16.  
 XX  
 PT Novel anti-inflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 CC  
 CC The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC anti-inflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,  
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antihypertensive, virostatic and anti-allergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
 CC lupus, polymyositis, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

CC Sequence 7 AA;

Query Match 100.0%; Score 40; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 1 ADMSWA 6

RESULT 6

ID ADA61850 standard; peptide; 7 AA.

AC ADA61850;

DT 20-NOV-2003 (first entry)

DE NF-kB essential modulator (NEMO) binding peptide #50.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
 XX anti-inflammatory; antiasthmatic; antipneumonia; antihypertensive;  
 XX dermatologic; osteoporosis; antibacterial; immunosuppressive;  
 XX gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 XX psoriasis; rheumatoid arthritis; osteoarthritis;  
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
 XX systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 XX Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 XX necrosis factor kappa B essential modulator.

XX Unidentified.

PN US2003054999-A1.

XX 20-MAR-2003.

PF 02-MAY-2001; 2001US-00847946.

PR 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

XX (HANN/) HANNIG G.

PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
 PT cancer, comprises a membrane translocation domain and a NEMO binding  
 PT sequence.

PS Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (i). The  
 CC compound is useful for diagnosing or treating inflammatory disorders,  
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
 CC Alzheimer's disease or viral infection. This is the amino acid sequence  
 CC of an anti-inflammatory peptide that binds to, and down-regulates,  
 CC necrosis factor kappa B (NF-kB) essential modulator (NEMO).

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 1 ADMSWA 6

RESULT 7

ID AAM48575 standard; peptide; 8 AA.

AC AAM48575;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 78.

XX Anti-inflammatory; cytostatic; antipneumonia; nootropic;  
 XX anti-inflammatory; antiasthmatic; osteoporosis; antibacterial; virostatic;  
 XX immunosuppressive; dermatological; neuroprotective; antihypertensive;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

PA (PRAE-) PRAECLIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel anti-inflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC anti-inflammatory compounds have antiaesthetic, cytostatic, antipneumonia,  
 CC antihypertensive, antiasthmatic, osteoporosis, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NfkappaB activation by  
 CC blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikappab. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||  
 DB 1 ADMSWA 6

RESULT 8  
 AAM48567  
 ID AAM48567 standard; peptide; 8 AA.  
 AC AAM48567;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 70.  
 XX  
 XX Antinflammatory; antiasthmatic; cytostatic; antiporiatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; Nfkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US014346.  
 PF  
 XX 02-MAY-2000; 2000US-0201261P.  
 PR 22-AUG-2000; 2000US-00643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI  
 XX May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX WPI; 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.  
 XX  
 XX Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC antiinflammatory compounds have antiasthmatic, cytostatic, antiporiatic,  
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated Nfkappab activation by  
 CC blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikappab. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||  
 DB 3 ADMSWA 8

RESULT 9  
 ADA61851  
 ID ADA61851 standard; peptide; 8 AA.  
 AC ADA61851;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX  
 DE NFkB essential modulator (NEMO) binding peptide #51.  
 XX  
 XX NEMO binding domain; NBP; I kappa B kinase beta; IKKbeta;  
 KW antinflammatory; antiasthmatic; antiporiatic; antirheumatic;  
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
 KW dermatological; neuroprotective; cytostatic; nootropic; virucide;  
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 KW psoriasis; rheumatoid arthritis; osteoarthritis;  
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 KW necrosis factor kappa B essential modulator.  
 XX  
 XX Unidentified.  
 OS  
 XX US2003054999-A1.  
 PN  
 XX 20-MAR-2003.  
 PD  
 XX  
 XX 02-MAY-2001; 2001US-00847946.  
 PF  
 XX 02-MAY-2000; 2000US-0201261P.  
 PR  
 XX  
 XX (MAYW/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 PA (FINDEIS) FINDEIS M A.  
 PA (PHILLIPS) PHILLIPS K.  
 PA (HANNING) HANNING G.  
 PI  
 XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
 XX WPI; 2003-596541/56.  
 DR  
 XX New compound for diagnosing or treating inflammatory disorders, e.g.  
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding  
 XX sequence.  
 PS Claim 6; Page 23; 37pp; English.  
 XX  
 CC The invention describes an anti-inflammatory compound comprising (I). The  
 CC compound is useful for diagnosing or treating inflammatory disorders,  
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
 CC Alzheimer's disease or viral infection. This is the amino acid sequence  
 CC of an anti-inflammatory peptide that binds to, and down-regulates,  
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
 XX  
 SO Sequence 8 AA;

Query Match 100.0%; Score 40; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 1 ADMSWA 6

RESULT 10  
 ADA61843 standard; peptide; 8 AA.

AC ADA61843;  
 XX 20-NOV-2003 (first entry)  
 DE NFkB essential modulator (NEMO) binding peptide #43.

XX NEMO binding domain; NBD, I kappa B kinase beta, IKKbeta;  
 XX antiinflammatory; antiasthmatic; antipsoiatic; antirheumatic;  
 XX antiarthritic; osteopathic; antibacterial; immunosuppressive;  
 XX dermatological; neuroprotective; cyostatic; nootropic; vitrucide;  
 XX gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 XX psoriasis; rheumatoid arthritis; osteoarthritis; autoimmune disease;  
 XX inflammatory bowel disease; sepsis; vasculitis; cancer; osteoporosis;  
 XX systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 XX Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 XX necrosis factor kappa B essential modulator.

OS Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.  
 XX (GHOS/) GHOSH S.  
 XX (FINND/) FINDEIS M A.  
 XX (PHIL/) PHILLIPS K.  
 XX (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
 PT cancer, comprises a membrane translocation domain and a NEMO binding  
 PT sequence.

PS Claim 6; Page 23; 37pp; English.

CC The invention describes an anti-inflammatory compound comprising (I). The  
 CC compound is useful for diagnosing or treating inflammatory disorders,  
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
 CC Alzheimer's disease or viral infection. This is the amino acid sequence  
 CC of an anti-inflammatory peptide that binds to, and down-regulates,  
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
 XX  
 SO Sequence 8 AA;

Query Match 100.0%; Score 40; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 3 ADMSWA 8

RESULT 11  
 AAM48573 standard; peptide; 9 AA.

AC AAM48573;  
 XX 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 76.

XX Antiinflammatory; antiasthmatic; cyostatic; antipsoiatic; nootropic;  
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; vitrucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 89pp; English.

XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC antiinflammatory compounds have antiasthmatic, cyostatic, antipsoiatic,  
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antiatherosclerotic, vitrucide and anti-allergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NFkappaB activation by



CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC antiinflammatory compounds have antiasthmatic, cytoskeletal, antipsoriatic,  
 CC antiinflammatory, antiarthritic, osteoprotective, neurotrophic,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of I-kappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of I-kappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

SO Sequence 9 AA;  
 Query Match 100.0%; Score 40; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 Db 1 ADMSWA 6

RESULT 14  
 AAM48572  
 ID AAM48572 standard; peptide; 9 AA.  
 AC AAM48572;  
 DT 20-MAR-2002 (first entry)  
 XX  
 XX Anti-inflammatory peptide SEQ ID NO 75.  
 DE  
 XX  
 XX Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;  
 XX antiinflammatory; antiarthritic; osteoprotective; antibacterial; virocidic;  
 XX immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 XX antiinflammatory; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX WO200183554-A2.  
 PN  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US014346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-0201261P.  
 PR  
 XX 22-AUG-2000; 2000US-00643260.  
 PR  
 XX  
 XX (PRAE-) PRACIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PA  
 XX May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 XX WPI; 2002-121869/16.  
 DR  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.

XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
 CC antiinflammatory compounds have antiasthmatic, cytoskeletal, antipsoriatic,  
 CC antiinflammatory, antiarthritic, osteoprotective, neurotrophic,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of I-kappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of I-kappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis

SO Sequence 9 AA;  
 Query Match 100.0%; Score 40; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 Db 3 ADMSWA 8

RESULT 15  
 ADA61848  
 ID ADA61848 standard; peptide; 9 AA.  
 AC ADA61848;  
 DT 20-NOV-2003 (first entry)  
 XX  
 XX NF-kB essential modulator (NEMO) binding peptide #48.  
 DE  
 XX  
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
 XX antiinflammatory; antiasthmatic; antipsoriatic; antineumatic;  
 XX antiarthritic; osteoprotective; antibacterial; immunosuppressive;  
 XX dermatological; neuroprotective; cytoskeletal; nootropic; virocidic;  
 XX gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
 XX psoriasis; rheumatoid arthritis; osteoarthritis;  
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
 XX systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
 XX Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
 XX necrosis factor kappa B essential modulator.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX US2003054999-A1.  
 PN  
 XX  
 XX 20-MAR-2003.  
 PD  
 XX  
 XX 02-MAY-2001; 2001US-00847946.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-0201261P.  
 PR  
 XX  
 XX (MAYM/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 PA (FINDEIS) FINDEIS M A.  
 PA (PHIL/) PHILLIPS K.  
 PA (HANN/) HANNIG G.  
 XX



PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX

PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX

PS Claim 6; Page 23; 37pp; English.  
XX

XX The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||  
|||  
|||  
Db 3 ADMSWA 8

Search completed: April 26, 2004, 13:07:32  
Job time : 56 secs

This Page Blank (uspto)

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:08:54 ; Search time 42 Seconds  
(without alignments)  
39.496 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues  
Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 40    | 100.0       | 6      | 10    | US-09-847-946A-41  |
| 2          | 40    | 100.0       | 6      | 10    | US-09-847-946A-73  |
| 3          | 40    | 100.0       | 7      | 10    | US-09-847-946A-77  |
| 4          | 40    | 100.0       | 8      | 10    | US-09-847-946A-78  |
| 5          | 40    | 100.0       | 8      | 10    | US-09-847-946A-78  |
| 6          | 40    | 100.0       | 9      | 10    | US-09-847-946A-69  |
| 7          | 40    | 100.0       | 9      | 10    | US-09-847-946A-72  |
| 8          | 40    | 100.0       | 9      | 10    | US-09-847-946A-75  |
| 9          | 40    | 100.0       | 9      | 10    | US-09-847-946A-76  |
| 10         | 40    | 100.0       | 10     | 10    | US-09-847-946A-71  |
| 11         | 40    | 100.0       | 10     | 10    | US-09-847-946A-74  |
| 12         | 40    | 100.0       | 11     | 10    | US-09-847-946A-68  |
| 13         | 37    | 92.5        | 236    | 12    | US-10-441-625-17   |
| 14         | 37    | 92.5        | 236    | 14    | US-10-441-625-17   |
| 15         | 37    | 92.5        | 885    | 9     | US-09-815-242-5090 |

|    |    |      |     |    |                      |                   |
|----|----|------|-----|----|----------------------|-------------------|
| 16 | 37 | 92.5 | 885 | 12 | US-10-282-132A-43572 | Sequence 43572, A |
| 17 | 36 | 90.0 | 6   | 9  | US-09-847-940B-4     | Sequence 4, Appl  |
| 18 | 36 | 90.0 | 6   | 9  | US-09-847-940B-5     | Sequence 5, Appl  |
| 19 | 36 | 90.0 | 6   | 10 | US-09-847-946A-4     | Sequence 4, Appl  |
| 20 | 36 | 90.0 | 6   | 10 | US-09-847-946A-5     | Sequence 5, Appl  |
| 21 | 36 | 90.0 | 6   | 10 | US-09-847-946A-39    | Sequence 39, Appl |
| 22 | 36 | 90.0 | 6   | 10 | US-09-847-946A-40    | Sequence 40, Appl |
| 23 | 36 | 90.0 | 6   | 10 | US-09-847-946A-51    | Sequence 51, Appl |
| 24 | 36 | 90.0 | 6   | 10 | US-09-847-946A-62    | Sequence 62, Appl |
| 25 | 36 | 90.0 | 7   | 10 | US-09-847-946A-55    | Sequence 55, Appl |
| 26 | 36 | 90.0 | 7   | 10 | US-09-847-946A-66    | Sequence 66, Appl |
| 27 | 36 | 90.0 | 8   | 10 | US-09-847-946A-48    | Sequence 48, Appl |
| 28 | 36 | 90.0 | 8   | 10 | US-09-847-946A-56    | Sequence 56, Appl |
| 29 | 36 | 90.0 | 8   | 10 | US-09-847-946A-59    | Sequence 59, Appl |
| 30 | 36 | 90.0 | 8   | 10 | US-09-847-946A-67    | Sequence 67, Appl |
| 31 | 36 | 90.0 | 9   | 10 | US-09-847-946A-47    | Sequence 47, Appl |
| 32 | 36 | 90.0 | 9   | 10 | US-09-847-946A-50    | Sequence 50, Appl |
| 33 | 36 | 90.0 | 9   | 10 | US-09-847-946A-53    | Sequence 53, Appl |
| 34 | 36 | 90.0 | 9   | 10 | US-09-847-946A-54    | Sequence 54, Appl |
| 35 | 36 | 90.0 | 9   | 10 | US-09-847-946A-58    | Sequence 58, Appl |
| 36 | 36 | 90.0 | 9   | 10 | US-09-847-946A-61    | Sequence 61, Appl |
| 37 | 36 | 90.0 | 9   | 10 | US-09-847-946A-64    | Sequence 64, Appl |
| 38 | 36 | 90.0 | 9   | 10 | US-09-847-946A-65    | Sequence 65, Appl |
| 39 | 36 | 90.0 | 10  | 10 | US-09-847-946A-49    | Sequence 49, Appl |
| 40 | 36 | 90.0 | 10  | 10 | US-09-847-946A-52    | Sequence 52, Appl |
| 41 | 36 | 90.0 | 10  | 10 | US-09-847-946A-57    | Sequence 57, Appl |
| 42 | 36 | 90.0 | 10  | 10 | US-09-847-946A-60    | Sequence 60, Appl |
| 43 | 36 | 90.0 | 10  | 10 | US-09-847-946A-63    | Sequence 63, Appl |
| 44 | 36 | 90.0 | 11  | 10 | US-09-847-946A-46    | Sequence 46, Appl |
| 45 | 36 | 90.0 | 147 | 12 | US-10-424-599-199086 | Sequence 199086,  |

#### ALIGNMENTS

RESULT 1  
US-09-847-946A-41  
; Sequence 41, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
; OTHER INFORMATION: sequence  
; US-09-847-946A-41

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 2

US-09-847-946A-73  
; Sequence 73, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamnig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-73

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 3

US-09-847-946A-77  
; Sequence 77, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamnig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 77  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

Db 1 ADMSWA 6

RESULT 4  
US-09-847-946A-70  
; Sequence 70, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamnig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 3 ADMSWA 8

RESULT 5  
US-09-847-946A-78  
; Sequence 78, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamnig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-78

Query Match 100.0%; Score 40; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

## RESULT 6

US-09-847-946A-69  
; Sequence 69, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 69  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

## RESULT 7

US-09-847-946A-72  
; Sequence 72, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-72

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

## RESULT 8

US-09-847-946A-75  
; Sequence 75, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 3 ADMSWA 8

## RESULT 9

US-09-847-946A-76  
; Sequence 76, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-76

OTHER INFORMATION: sequence  
US-09-847-946A-76

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 2 ADWSMA 7

RESULT 10

US-09-847-946A-71  
Sequence 71, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamng, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 71  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-71

Query Match 100.0%; Score 40; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 2 ADWSMA 7

RESULT 11

US-09-847-946A-74  
Sequence 74, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamng, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 74  
LENGTH: 10  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-74

Query Match 100.0%; Score 40; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 3 ADWSMA 8

RESULT 12

US-09-847-946A-68  
Sequence 68, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamng, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-68

Query Match 100.0%; Score 40; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 3 ADWSMA 8

RESULT 13

US-10-441-625-17  
Sequence 17, Application US/10441625  
Publication No. US20030203467A1  
GENERAL INFORMATION:  
APPLICANT: Gualfetti, Peter  
APPLICANT: Mitchinson, Colin  
APPLICANT: Phillips, Jay Ian  
TITLE OF INVENTION: Novel Variant Egr1-Like Cellulase  
FILE REFERENCE: GC631  
CURRENT APPLICATION NUMBER: US/10/441,625  
CURRENT FILING DATE: 2003-05-19  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Gliocladium roseum (3)  
US-10-441-625-17

Query Match 92.5%; Score 37; DB 12; Length 236;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||:  
Db 63 ADMSWS 68

RESULT 14  
US-10-441-626-17  
; Sequence 17, Application US/10441626  
; Publication No. US20030186418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Phillips, Jay Ian  
; TITLE OF INVENTION: No. US20030186418A1 Variant EGIII-Like Cellulase  
; FILE REFERENCE: GC631  
; CURRENT APPLICATION NUMBER: US/10/441,626  
; CURRENT FILING DATE: 2003-05-19  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Gliocladium roseum (3)  
US-10-441-626-17

Query Match 92.5%; Score 37; DB 14; Length 236;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||:  
Db 63 ADMSWS 68

RESULT 15  
US-09-815-242-5090  
; Sequence 5090, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA 011a  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5090  
; LENGTH: 885  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||:  
Db 563 ADMSWA 568

Search completed: April 26, 2004, 13:14:32  
Job time : 42 secs

**This Page Blank (uspto)**

**This Page Blank (uspto)**

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:03:18 ; Search time 39 Seconds  
(without alignments)  
48.541 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 37    | 92.5        | 236    | 3  | Q8N1Y9      |
| 2          | 37    | 92.5        | 274    | 16 | Q8G6S9      |
| 3          | 37    | 92.5        | 375    | 5  | Q86KS0      |
| 4          | 37    | 92.5        | 437    | 16 | Q92K30      |
| 5          | 37    | 92.5        | 548    | 16 | Q92M15      |
| 6          | 37    | 92.5        | 581    | 5  | Q8MSH3      |
| 7          | 37    | 92.5        | 597    | 5  | Q9VGP2      |
| 8          | 37    | 92.5        | 610    | 16 | Q86712      |
| 9          | 37    | 92.5        | 885    | 16 | Q91389      |
| 10         | 36    | 90.0        | 173    | 16 | Q82SE1      |
| 11         | 36    | 90.0        | 205    | 16 | Q9ACR5      |
| 12         | 36    | 90.0        | 227    | 4  | Q81XK8      |
| 13         | 36    | 90.0        | 228    | 8  | Q7IGU8      |
| 14         | 36    | 90.0        | 242    | 12 | Q919K8      |
| 15         | 36    | 90.0        | 355    | 11 | Q8B1T9      |
| 16         | 36    | 90.0        | 358    | 10 | O50002      |

|    |    |      |      |    |        |
|----|----|------|------|----|--------|
| 17 | 36 | 90.0 | 374  | 16 | Q9H210 |
| 18 | 36 | 90.0 | 426  | 5  | Q86KF9 |
| 19 | 36 | 90.0 | 433  | 16 | Q8P4A1 |
| 20 | 36 | 90.0 | 438  | 16 | Q8P4V8 |
| 21 | 36 | 90.0 | 452  | 4  | Q96AB7 |
| 22 | 36 | 90.0 | 463  | 5  | Q8MMJ0 |
| 23 | 36 | 90.0 | 470  | 12 | Q7TF27 |
| 24 | 36 | 90.0 | 477  | 11 | Q9CYU6 |
| 25 | 36 | 90.0 | 484  | 4  | Q9BRV6 |
| 26 | 36 | 90.0 | 605  | 16 | Q82MX2 |
| 27 | 36 | 90.0 | 686  | 16 | Q8FQZ9 |
| 28 | 36 | 90.0 | 861  | 16 | Q8BNQ1 |
| 29 | 36 | 90.0 | 889  | 16 | Q9AAZ6 |
| 30 | 36 | 90.0 | 1005 | 16 | Q9XGZ2 |
| 31 | 36 | 90.0 | 1324 | 16 | Q820F9 |
| 32 | 36 | 90.0 | 5435 | 2  | Q9LAX2 |
| 33 | 35 | 87.5 | 527  | 16 | Q829Q9 |
| 34 | 35 | 85.0 | 166  | 4  | Q8NBW1 |
| 35 | 34 | 85.0 | 273  | 10 | Q94JM4 |
| 36 | 34 | 85.0 | 273  | 10 | Q940D6 |
| 37 | 34 | 85.0 | 275  | 10 | Q65710 |
| 38 | 34 | 85.0 | 337  | 11 | Q80UX8 |
| 39 | 34 | 85.0 | 376  | 3  | Q90VL4 |
| 40 | 34 | 85.0 | 617  | 10 | P93050 |
| 41 | 34 | 85.0 | 1074 | 16 | Q8BJ70 |
| 42 | 34 | 85.0 | 1842 | 3  | Q96WT6 |
| 43 | 34 | 85.0 | 1842 | 3  | Q96WT7 |
| 44 | 34 | 85.0 | 1842 | 3  | Q96WT8 |
| 45 | 33 | 82.5 | 49   | 6  | Q8SPL6 |

#### ALIGNMENTS

RESULT 1

Q8N1Y9 PRELIMINARY; PRT; 236 AA.

AC Q8N1Y9; ID Q8N1Y9

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endoglucanase.

GN CEL12C.

OS Bionectria ochroleuca (Glucoladium roseum).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.

OX NCBI\_TaxID=29856;

RP [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22067395; PubMed=12073090;

RA Goedegebuur F., Fowler T., Phillips J., van der Kley P., van Solingen P., Dankmeyer L., Power S.D.;

RT "Cloning and relational analysis of 15 novel fungal endoglucanases from family 12 glycosyl hydrolase."

RL Curr. Genet. 41:89-98(2002).

DR EMBL: AF435065; AAM77708.1;

DR GO: GO:000810; Fibrinolytic activity; IEA.

DR GO: GO:000272; Polysaccharide catabolism; IEA.

DR InterPro: IPR008985; ConA\_like\_1ec.gi.

DR Pfam: PF01670; Glyco\_hydro\_12; 1.

DR ProDom: PD004316; Glyco\_hydro\_12; 1.

SQ SEQUENCE 236 AA; 26024 MW; C3DBA7B33F0C4D8 CRC64;

Query Match 92.5%; Score 37; DB 3; Length 236;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 63 ADMSWS 68

```

RESULT 2
Q8G659 PRELIMINARY; PRT; 274 AA.
AC Q8G659;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Probable dihydroxyacetate dehydrogenase electron transfer subunit.
GN PYR OR BL0790.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karamirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AB014701; AAN24605.1; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008333; PAD binding_6.
DR Pfam; PF00970; PAD_binding_6; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 16; Length 274;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 171 ADMSWS 176

RESULT 3
Q8KX50 PRELIMINARY; PRT; 375 AA.
AC Q8KX50;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Dicyostelium discoideum (Slime mold).
DE Hypochemical protein.
OS Dicyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dicyostelidae; Dicyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szatranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox B., Onail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dicyostelium discoideum.";
RT Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RP Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC11612; AA050929.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000581; ILVD_EDD_family.
DR InterPro; IPR006970; PT.
DR Pfam; PF04886; PT; 1.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
KW Hypochemical protein.

```

```

SQ SEQUENCE 375 AA; 41862 MW; EC9A1D744C56856E CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 5; Length 375;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 46 SDMSWA 51

RESULT 4
Q92K30 PRELIMINARY; PRT; 437 AA.
ID Q92K30;
AC Q92K30;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Hypochemical protein R02283.
GN R02283 OR SMC01671.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46862.1; -
DR Hypochemical protein; Complete proteome.
KW SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 16; Length 437;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 157 ADMNWA 162

RESULT 5
Q92MT5 PRELIMINARY; PRT; 548 AA.
ID Q92MT5;
AC Q92MT5;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Putative fatty-acid-CoA ligase protein (BC 6.-.-.-).
GN R02631 OR SMC00741.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL: AL591791; CAC47210.1; -.  
 DR GO: GO:0016020; C-membrane; IEA.  
 DR GO: GO:0005524; F-ATP binding; IEA.  
 DR GO: GO:0004009; F-ATP-binding cassette (ABC) transporter acti. .; IEA.  
 DR GO: GO:0016874; F-ligase activity; IEA.  
 DR GO: GO:0008152; P-metabolism; IEA.  
 DR GO: GO:0006810; P-transport; IEA.  
 DR InterPro: IPR003439; ABC transporter.  
 DR InterPro: IPR000873; AMP-bind.  
 DR Pfam: PF00501; AMP-binding; 1.  
 DR PROSITE: PS00211; ABC TRANSPORTER\_1; 1.  
 DR PROSITE: PS00455; AMP BINDING; 1.  
 DR KW Ligase; Complete proteome.  
 SO SEQUENCE 548 AA; 59383 MW; 659A68C546EA53B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
 Db 235 ADMSWA 240

## RESULT 6

ID O8MSH3 PRELIMINARY; PRT; 581 AA.  
 AC O8MSH3;  
 DT 01-OCT-2002 (TEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE GH24640P  
 GN NINAG OR CG6728.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo K., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinkner S.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY118818; AAM50678.1; -.  
 DR FlyBase: FBgn0037896; ninag.  
 DR GO: GO:0004197; F-cysteine-type endopeptidase activity; IEA.  
 DR GO: GO:0016491; F-oxidoreductase activity; IEA.  
 DR GO: GO:0006118; P-electron transport; IEA.  
 DR GO: GO:0006508; P-proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000172; GMC\_oxred.  
 DR InterPro: IPR007867; GMC\_oxred.  
 DR InterPro: IPR000169; SHPTC\_acstite.  
 DR Pfam: PF05199; GMC\_oxred\_C; 1.  
 DR Pfam: PF00732; GMC\_oxred\_N; 1.  
 DR PROSITE: PS00639; THIOLE PROTEASE HIS; 1.  
 SO SEQUENCE 581 AA; 63475 MW; A2F13BBEC25B496D CRC64;

Query Match 92.5%; Score 37; DB 5; Length 581;  
 Best Local Similarity 83.3%; Pred. No. 5.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
 Db 158 SDMSWA 163

## RESULT 7

O9VGP2  
 ID O9VGP2 PRELIMINARY; PRT; 597 AA.  
 AC O9VGP2;  
 DT 01-MAY-2000 (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE CG6728 protein.  
 GN NINAG OR CG6728.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gottell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,  
 RA Jalali M., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maitre B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshirei A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Snue B.C., Siden-Kiamos I., Simpston W., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
 RA Svirskas R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Maassman D.A., Weinstock G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003691; AAP54634.1; -.  
 DR FlyBase: FBgn0037896; ninag.  
 DR GO: GO:0004197; F-cysteine-type endopeptidase activity; IEA.  
 DR GO: GO:0016491; F-oxidoreductase activity; IEA.  
 DR GO: GO:0006118; P-electron transport; IEA.  
 DR GO: GO:0006508; P-proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000172; GMC\_oxred.  
 DR InterPro: IPR007867; GMC\_oxred.  
 DR InterPro: IPR000169; SHPTC\_acstite.  
 DR Pfam: PF05199; GMC\_oxred\_C; 1.  
 DR Pfam: PF00732; GMC\_oxred\_N; 1.  
 DR PROSITE: PS00639; THIOLE PROTEASE HIS; 1.  
 DR PROSITE: PS00639; THIOLE PROTEASE HIS; 2; 1.  
 SO SEQUENCE 597 AA; 65274 MW; 8C4C362AFRA0902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;  
 Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
DB 158 SDMSWA 163

RESULT 8  
ID 086712 PRELIMINARY; PRT; 610 AA.  
AC 086712;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein SC06530.  
GN SC06530 OR SC5C7.15;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,  
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2)."  
RL Nature 417:141-147(2002).  
DR EMBL: AL939128; CAA20627.1; -.  
DR PIR: T35222; T35222.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 610;  
Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
DB 83 ADMSWA 88

RESULT 9  
ID 091389 PRELIMINARY; PRT; 885 AA.  
AC 091389;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Two-component sensor Kdp.  
GN KDPD OR PA1636.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RX MEDLINE=20437337; PubMed=10994043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.J., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Tolentino R., Westbrook-Adams S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Saiter W.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
CC -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.  
DR EMBL: AE004591; AM05025.1; -.  
DR PIR: C83441; C83441.  
DR HSSP: P02933; 1UOT.  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0005524; P:ATP binding; IEA.  
DR GO: GO:0016301; P:kinase activity; IEA.  
DR GO: GO:0016740; P:kinase activity; IEA.  
DR GO: GO:0000155; P:two-component sensor molecule activity; IEA.  
DR GO: GO:0006950; P:response to stress; IEA.  
DR GO: GO:0007600; P:sensory perception; IEA.  
DR GO: GO:007165; P:signal transduction; IEA.  
DR InterPro: IPR003594; ATPbind ATPase.  
DR InterPro: IPR004358; Bact\_sens\_pr\_C.  
DR InterPro: IPR003018; GAF.  
DR InterPro: IPR005467; His\_kinase.  
DR InterPro: IPR003661; His\_kin\_N.  
DR InterPro: IPR003852; KdpD.  
DR InterPro: IPR06016; Usp\_dom.  
DR Pfam: PF02518; HATPase\_c1.  
DR Pfam: PF00512; HisKA\_1.  
DR Pfam: PF02702; KdpD; 1.  
DR Pfam: PF00582; Usp; 1.  
DR PRINTS: PR00344; BCTRLSENSOR.  
DR PRODOM: PD011725; KdpD; 1.  
DR SMART: SM00065; GAF; 1.  
DR SMART: SM00387; HATPase\_C; 1.  
DR SMART: SM00388; HisKA\_1.  
DR SMART: PS50109; His\_KIN; 1.  
DR KINASE: P550109; His\_KIN; 1.  
KW Kinase; Phosphorylation; Sensory transduction; Transferase;  
KW Complete proteome.  
SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;  
Best Local Similarity 83.3%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
DB 563 ADMSWA 568

RESULT 10  
ID 0825E1 PRELIMINARY; PRT; 173 AA.  
AC 0825E1;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN SAV7517.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
avermitilis: deducing the ability of producing secondary  
metabolites.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,

RA Sakaki Y., Hattori M., Omura S.;  
 RT "Complete genome sequence and comparative analysis of the industrial  
 microorganism *Streptomyces avermitilis*.";  
 RL Nat. Biotechnol. 21:526-531(2003).  
 DR EMBL: AP005050; BAC75228.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 173 AA; 18912 MW; 22B26C7D2222CA60 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 173;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 53 ADMSWA 58

RESULT 11  
 ID 09ACR5 PRELIMINARY; PRT; 205 AA.

AC 09ACR5;  
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
 DE Hypothetical protein SCPI.253.  
 GN SCPI.253.  
 OS Streptomyces coelicolor.  
 OC Plasmid SCPI.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cardeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,  
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wieruszka A., Woodward J., Barrall B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces*  
*coelicolor* A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL590464; CAC36779.1; -  
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 10 ADMSW 14

RESULT 12

ID 081XK8 PRELIMINARY; PRT; 227 AA.

AC 081XK8;  
 RC STRAIN=2003 (T-EMBLrel. 23, Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DE Similar to hypothetical protein BC017335.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC040173; AAH40173.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 113 ADMSW 117

RESULT 13

ID 07YU8 PRELIMINARY; PRT; 228 AA.

AC 07YU8;  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DE Cytochrome oxidase subunit II.  
 OS Sphenodon punctatus (Tuatara).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.  
 OX NCBI\_TaxID=8508;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rest J.S., Ast J.C., Austin C.C., Waddell P.J., Tibbetts E.A.,  
 RA Hay J.M., Mindell D.P.;  
 RT "Molecular systematics of primary reptilian lineages and the tuatara  
 mitochondrial genome.";  
 RL Mol. Phylogenet. Evol. 0:0-0(2003).  
 DR EMBL: AF534390; AAP42708.1; -  
 KW Mitochondrion.  
 SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;

Query Match 90.0%; Score 36; DB 8; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
 DB 221 DMSWA 225

RESULT 14

ID 0919K8 PRELIMINARY; PRT; 242 AA.

AC 0919K8;  
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DE CUN068 hypothetical protein.  
 GN CUN068.  
 OS Culex nigripalpus baculovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
 OX NCBI\_TaxID=130556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Florida1997;  
 RX MEDLINE=21488685; PubMed=11602755;  
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.;  
 RT "Genome Sequence of a Baculovirus Pathogenic for *Culex nigripalpus*.";  
 RL J. Virol. 75:11157-11165(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Florida1997;  
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.;  
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL:AF403738; AAK94146.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 242 AA; 27222 MW; 601496753110B52 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
 |||||  
 Db 80 DMSWA 84

RESULT 15  
 Q8BIT9 PRELIMINARY; PRT; 355 AA.  
 ID Q8BIT9  
 AC Q8BIT9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mitochondrial ribosomal protein L41 homolog.  
 GN 2810443J12RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The PANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 DR EMBL:AK087998; BAC40084.1; -  
 DR MGI:1914478; 2810443J12RIK.  
 DR InterPro: IPR001680; WD40.  
 DR SMART; SM00320; WD40; 4.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 SQ SEQUENCE 355 AA; 40183 MW; FBF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 |||||  
 Db 215 ADMSW 219

Search completed: April 26, 2004, 13:08:48  
 Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:04:13 ; Search time 21 Seconds  
(without alignments)  
27.483 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADMSMA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 37    | 92.5        | 610    | 2     | T35222 hypothetical prote |
| 2          | 37    | 92.5        | 885    | 2     | C83441 two-component sens |
| 3          | 36    | 90.0        | 374    | 2     | B83241 conserved hypothet |
| 4          | 36    | 90.0        | 889    | 2     | E87304 TonB-dependent rec |
| 5          | 34    | 85.0        | 275    | 2     | T05822 hypothetical prote |
| 6          | 34    | 85.0        | 617    | 2     | C84922 probable protein k |
| 7          | 34    | 85.0        | 1842   | 2     | T43409 probable fatty-aci |
| 8          | 34    | 85.0        | 1842   | 2     | T38781 fatty acid synthas |
| 9          | 33    | 82.5        | 132    | 2     | B65785 mel-13a protein -  |
| 10         | 33    | 82.5        | 198    | 2     | B82531 conserved hypothet |
| 11         | 33    | 82.5        | 220    | 2     | D64316 restriction modifi |
| 12         | 33    | 82.5        | 232    | 2     | S58353 CD1b protein - she |
| 13         | 33    | 82.5        | 239    | 2     | D90470 hypothetical prote |
| 14         | 33    | 82.5        | 257    | 2     | D87152 conserved hypothet |
| 15         | 33    | 82.5        | 276    | 2     | B75337 hypothetical prote |
| 16         | 33    | 82.5        | 304    | 2     | F83632 probable cytochrom |
| 17         | 33    | 82.5        | 310    | 2     | JC7853 L-fucose-specific  |
| 18         | 33    | 82.5        | 324    | 2     | AB3548 vegetatible incomp |
| 19         | 33    | 82.5        | 328    | 2     | E72424 oligopeptide ABC t |
| 20         | 33    | 82.5        | 333    | 2     | S47246 gene CD1 protein - |
| 21         | 33    | 82.5        | 350    | 2     | S71923 cysteine proteinas |
| 22         | 33    | 82.5        | 368    | 2     | H90998 probable proteinas |
| 23         | 33    | 82.5        | 410    | 2     | D75475 lycopene cyclase - |
| 24         | 33    | 82.5        | 415    | 2     | AE1844 hypothetical prote |
| 25         | 33    | 82.5        | 418    | 2     | AE1460 sugar ABC transpor |
| 26         | 33    | 82.5        | 418    | 2     | AF1097 sugar ABC transpor |
| 27         | 33    | 82.5        | 421    | 2     | T38242 probable phosphata |
| 28         | 33    | 82.5        | 433    | 2     | T31511 hypothetical prote |
| 29         | 33    | 82.5        | 467    | 2     | G82697 hypothetical prote |

|    |    |      |      |   |                            |
|----|----|------|------|---|----------------------------|
| 30 | 33 | 82.5 | 478  | 2 | E89790 6-phospho-beta-glu  |
| 31 | 33 | 82.5 | 479  | 2 | I19953 6-phospho-beta-glu  |
| 32 | 33 | 82.5 | 492  | 2 | S01098 aerolysin precursor |
| 33 | 33 | 82.5 | 529  | 2 | C86958 probable GMP synth  |
| 34 | 33 | 82.5 | 539  | 2 | T15256 hypothetical prote  |
| 35 | 33 | 82.5 | 578  | 2 | C64452 restriction modifi  |
| 36 | 33 | 82.5 | 590  | 2 | S72813 GMP synthase (glut  |
| 37 | 33 | 82.5 | 616  | 2 | C69226 type I restriction  |
| 38 | 33 | 82.5 | 623  | 2 | E75221 type I restriction  |
| 39 | 33 | 82.5 | 765  | 2 | S76795 hypothetical prote  |
| 40 | 33 | 82.5 | 836  | 2 | D82177 conserved hypothet  |
| 41 | 33 | 82.5 | 1202 | 2 | S71424 nitric-oxide synth  |
| 42 | 33 | 82.5 | 1203 | 1 | A47501 nitric-oxide synth  |
| 43 | 33 | 82.5 | 1205 | 1 | A38943 nitric-oxide synth  |
| 44 | 33 | 82.5 | 1329 | 1 | D87226 conserved hypothet  |
| 45 | 33 | 82.5 | 1409 | 2 | S74916 alkaline phosphata  |

## ALIGNMENTS

## RESULT 1

T35222 hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999

C/Accession: T35222

R/Seeger, K.V.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1998

A/Reference number: Z21572

A/Accession: T35222

A/Status: preliminary; translated from GB/EMBL/DDdbJ

A/Molecule type: DNA

A/Residues: 1-610 <SEB>

A/Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SC0EDB:SC5C7.15

A/Experimental source: strain A3(2)

A/Genetic:

A/Genes: SC0EDB:SC5C7.15

## Query Match

Best Local Similarity 92.5%; Score 37; DB 2; Length 610;

Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSMA 6  
Db 83 ADMAMA 88

## RESULT 2

C83441 two-component sensor kdpd PA1636 (imported) - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: C83441

R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj

adman, S.; Yan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog

A/Reference number: A82950; PMID:10984043

A/Accession: C83441

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-885 <STO>

A/Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AA05025.1; GSPDB:GN001;

A/Experimental source: strain PA01

C/Genetic:

A/Genes: kdpd; PA1636

Query Match 92.5%; Score 37; DB 2; Length 885;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||:|  
Db 563 ADMSWA 568

## RESULT 3

B83241

conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: B83241

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,

.i. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A/Reference number: A82950; WUID:2043737; PMID:10984043

A/Accession: B83241

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-374 <STO>

A/Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AA06618.1; GSPDB:GN001

A/Experimental source: strain PAO1

C/Genetics:

A/Gene: PA3230

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 374;  
Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||:|  
Db 81 DMSWA 85

## RESULT 4

E87304

TonB-dependent receptor [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C/Accession: E87304

R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kjol

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; WUID:21173698; PMID:11259647

A/Accession: E87304

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-889 <STO>

A/Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148

C/Genetics:

A/Gene: CC0446

Query Match

Best Local Similarity 100.0%; Score 36; DB 2; Length 889;  
Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:|  
Db 618 ADMSW 622

## RESULT 5

T05822

hypothetical protein TSK18.170 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999

C/Accession: T05822

R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba

submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15453

A/Accession: T05822

A/Molecule type: DNA

A/Residues: 1-275 <BEV>

A/Cross-references: EMBL:AL022580

A/Experimental source: cultivar Columbia; BAC clone TSK18

C/Genetics:

A/Map position: 4

A/Introns: 103/3; 141/3; 169/1; 206/3

A/Note: TSK18.170

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 275;  
Matches 4; Conservativity 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||:|  
Db 57 SDMSWS 62

## RESULT 6

C84922

probable protein kinase [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C/Accession: C84922

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyam, L.; Tallon, L.

enes, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; WUID:20083487; PMID:10617197

A/Accession: C84922

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-617 <STO>

A/Cross-references: GB:AE002093; NID:g4249408; PIDN:AA013705.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 617;  
Matches 4; Conservativity 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||:|  
Db 500 ADMSWA 505

## RESULT 7

T43409

probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy

N/Alternate names: fatty acid synthetase alpha subunit

C/Species: Schizosaccharomyces pombe

C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C/Accession: T43409

R/Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hiraata, A.; Yan

J. Cell Biol 134, 949-961, 1996

A/Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase and

A/Reference number: Z22493; WUID:96354912; PMID:8769419

A/Accession: T43409

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1642 <SAI>

A/Cross-references: EMBL:DB3412; NID:g1199959; PIDN:BA11913.1; PID:g1199960

C/Genetics:

A/Note: led1+

C/Superfamily: yeast fatty-acid synthase

C/Keywords: acyltransferase; coenzyme A

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 1642;  
Matches 4; Conservativity 2; Mismatches 0; Indels 0; Gaps 0;



QY 1 ADMSWA 6  
: : : :  
DB 400 SDMNMA 405

## RESULT 8

138781  
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
A/Accession: T38781  
R/Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A/Reference number: Z21751  
A/Accession: T38781  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1842 <SKE>  
A/Cross-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c  
A/Experimental source: strain 972h-; cosmid c4A8  
C/Genetics:  
A/Gene: SPDB:SPAC4A8.11c  
A/Map position: 1  
C/Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
: : : :  
DB 400 SDMNMA 405

## RESULT 9

S65785  
mel-13a protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
A/Accession: S65785  
R/Reteu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
Biochem. Biophys. Acta 1305, 109-112, 1996  
A/Title: Cloning and characterization of two transcripts generated from the mel-13 gene  
A/Reference number: S65785; MID:96180310; PMID:8597552  
A/Accession: S65785  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <TET>  
A/Cross-references: EMBL:U35309  
C/Genetics:  
A/Gene: mel-13  
C/Superfamily: mouse mel-13a protein  
C/Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
: : : :  
DB 57 SDMSW 61

## RESULT 10

B82531  
conserved hypothetical protein XF2666 (imported) - Xylella fastidiosa (strain 9a5c)  
C/Species: Xylella fastidiosa  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000  
A/Accession: B82531  
R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MID:20365717; PMID:10910347  
A/Note: for a complete list of authors see reference number A59328 below

A/Accession: B82531  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-198 <SIM>  
A/Cross-references: GB:AE004072; GB:AE003849; NID:G9107884; PIDN:AAF85463.1; GSPDB:GN001;  
A/Experimental source: strain 9a5c  
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al  
Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A/Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigre  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsuchioka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze  
A/Reference number: A59328  
A/Contents: annotation  
C/Genetics:  
A/Gene: XF2666  
C/Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
: : : :  
DB 135 DNMWA 139

## RESULT 11

D64316  
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii  
C/Species: Methanococcus jannaschii  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2002  
A/Accession: D64316  
R/Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.  
; Reich, C.I.; Overbeek, R.; Kirsnes, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A/Reference number: A64300; MID:96337999; PMID:8688087  
A/Accession: D64316  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-220 <BUL>  
A/Cross-references: GB:U67470; GB:L77117; NID:G2826247; PIDN:AAB98113.1; PID:G1592267; T  
C/Genetics:  
A/Map position: REV127472-126810  
C/Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
: : : :  
DB 33 ADMAW 37

## RESULT 12

S58353  
CDB protein - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
A/Accession: S58353

R.Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.  
submitted to the EMBL Data Library, July 1995  
A:Description: The ovine CD1 gene family contains at least four CD1B homologues.  
A:Reference number: S58353  
A:Accession: S58353  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-232 <PER>  
A:Cross-references: EMBL:X90567; NID:G945010; PIDN:CAA62187.1; PID:G945011  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:115-180/Domain: immunoglobulin homology <ITM>

Query Match 82.5%; Score 33; DB 2; Length 232;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 156 ADMTW 160

## RESULT 13

D90470  
hypothetical protein cyvH [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C:Accession: D90470  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-  
Jung, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.  
arrect, K.A.; Ragan, M.A.; Senema, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: D90470  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-239 <KUR>  
A:Cross-references: GB:AE006641; NID:G13816282; PIDN:AAK43019.1; GSPDB:GND00155  
C:Genetics:

A:Gene: cyvH  
C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 172 ADMTW 176

## RESULT 14

D87152  
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: D87152  
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-  
R.; Davies, R.M.; Devlin, K.; Dutroy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq  
A:Title: Massive gene decay in the leprosy bacillus.  
A:Reference number: A86909; MUID:21128732; PMID:11234002  
A:Accession: D87152  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-257 <STO>  
A:Cross-references: GB:AL450380; NID:G13093601; PIDN:CAC30900.1; GSPDB:GND00147  
C:Genetics:

A:Gene: ML1945  
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 11 ATMSWA 16

## RESULT 15

B75337  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: B75337  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ueberlack, T.; Zalewski, C.; Mah  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: B75337  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-276 <WHI>  
A:Cross-references: GB:AE002032; GB:AE000513; NID:G6459715; PIDN:AAF11479.1; PID:G6459711  
A:Experimental source: strain R1  
C:Genetics:

A:Gene: DR1923  
A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 84 ADMAW 88

Search completed: April 26, 2004, 13:09:21  
Job time : 22 secs



FT CARBOHYD 398 398 N-LINKED (GLCNAC.. ) (POTENTIAL).  
SQ SEQUENCE 470 AA; 51989 MW; D1A6F07460F68AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 453 ADMSW 457

RESULT 2  
NRAM\_IADCH STANDARD; PRT; 470 AA.

AC 007571;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_Taxid=38957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawaoka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A  
viruses.";  
RL Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
chains of the host cell surface proteins and from the viral  
envelope. Such a reaction prevents self-aggregation and facilitates  
the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
oligosaccharides, glycoproteins, glycolipids, colominic acid and  
synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped  
spike on the surface of the virion.  
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; L06573; AAA43372.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 275 275 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC.. ) (POTENTIAL).

SQ SEQUENCE 470 AA; 52070 MW; 169A89FBEB806DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 453 ADMSW 457

RESULT 3  
NRAM\_IADH2 STANDARD; PRT; 470 AA.

AC 007572;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_Taxid=11358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawaoka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A  
viruses.";  
RL Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
chains of the host cell surface proteins and from the viral  
envelope. Such a reaction prevents self-aggregation and facilitates  
the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
oligosaccharides, glycoproteins, glycolipids, colominic acid and  
synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped  
spike on the surface of the virion.  
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; L06574; AAA43372.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 275 275 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC.. ) (POTENTIAL).

SQ SEQUENCE 470 AA; 52015 MW; E1CID3E2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

Db 453 ADMSW 457

```

RESULT 4
NRAM_IADM2 STANDARD; PRT; 470 AA.
ID NRAM_IADM2 007573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OC NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of influenza A
RT viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L06575; AAA3404.1; -.
CC HSSP: P06820; 2BAT.
CC InterPro: IPR001860; Glyco_hydro_34.
CC Pfam: PF00064; neur. 1.
CC ProDom: PD000431; Glyco_hydro_34; 1.
CC Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
CC FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
CC FT ACT_SITE 273 273 BY SIMILARITY.
CC FT ACT_SITE 275 275 BY SIMILARITY.
CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 470 AA; 52146 MW; 30F5F9B364C1F49 CRC64;

```

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 Db 453 ADMSW 457

```

RESULT 5
NRAM_IADU3 STANDARD; PRT; 470 AA.
ID NRAM_IADU3 007559;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OC NCBI_TaxID=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of influenza A
RT viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L06576; AAA16234.1; -.
CC HSSP: P06820; 2BAT.
CC InterPro: IPR001860; Glyco_hydro_34.
CC Pfam: PF00064; neur. 1.
CC ProDom: PD000431; Glyco_hydro_34; 1.
CC Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM ANCHOR (BY SIMILARITY).
CC DOMAIN 38 88 HYPERVARIABLE STALK REGION.
CC FT DOMAIN 39 88 HEAD OF NEURAMINIDASE.
CC FT ACT_SITE 273 273 PROBABLE.
CC FT ACT_SITE 275 275 PROBABLE.
CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

```

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 Db 453 ADMSW 457

RESULT 6  
 NRAM\_IAGFN STANDARD; PRT; 470 AA.  
 ID NRAM\_IAGFN 007574;  
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA  
 OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=38963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 viruses";  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 CC chains of the host cell surface proteins and from the viral  
 CC envelope. Such a reaction prevents self-aggregation and facilitates  
 CC the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped  
 CC spike on the surface of the virion.  
 CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: L06584; AAA3428.1; -  
 CC HSSP: P06820; 2BAt.  
 DR InterPro: IPR001860; Glyco\_hydro\_34.  
 DR Pfam: PF00064; neur. 1.  
 KW Hydroxylase; Glycosidase; Glyco\_hydro\_34; 1.  
 DR ProDom: PD000431; Glyco\_hydro\_34; 1.  
 FT DOMAIN 7 38 ANCHOR (BY SIMILARITY).  
 FT TRANSMEM 7 38 HYPERVARIABLE STALK REGION.  
 FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.  
 FT ACT\_SITE 273 273 BY SIMILARITY.  
 FT ACT\_SITE 275 275 BY SIMILARITY.  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 470 AA; 52348 MW; D3BDAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 453 ADMSW 457  
 RESULT 7  
 NRAM\_IAGHD STANDARD; PRT; 470 AA.  
 AC 007577;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.

OS Influenza A virus (strain A/Herring gull/DE/677/88).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=38964;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 viruses";  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 CC chains of the host cell surface proteins and from the viral  
 CC envelope. Such a reaction prevents self-aggregation and facilitates  
 CC the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped  
 CC spike on the surface of the virion.  
 CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: L06585; AAA3368.1; -  
 CC HSSP: P06820; 2BAt.  
 DR InterPro: IPR001860; Glyco\_hydro\_34.  
 DR Pfam: PF00064; neur. 1.  
 KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.  
 DR ProDom: PD000431; Glyco\_hydro\_34; 1.  
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.  
 FT ACT\_SITE 273 273 BY SIMILARITY.  
 FT ACT\_SITE 275 275 BY SIMILARITY.  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 453 ADMSW 457  
 RESULT 8  
 NRAM\_IAGHD STANDARD; PRT; 470 AA.  
 AC 007578;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Equine/Jilliin/1/89).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=11401;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 chains of the host cell surface proteins and from the viral
 envelope. Such a reaction prevents self-aggregation and facilitate
 the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
 spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06579; AAA43374.1; -.
CC HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT CARBOHYD 46 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; C50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

```

```

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 chains of the host cell surface proteins and from the viral
 envelope. Such a reaction prevents self-aggregation and facilitate
 the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
 spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06586; AAA3369.1; -.
CC HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT CARBOHYD 46 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 10
ID NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side

```

chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.

-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

-1- SUBUNIT: Homotrimer.

-1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.

-1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL: L06588; AAA3410.1; -.

HSSP: P06820; 2BAT.

DR InterPro: IPR001860; Glyco\_hydro\_34.

DR Pfam: PF00664; neur; 1.

DR ProDom: PD000431; Glyco\_hydro\_34; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 273 273 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 470 AA; 52352 MW; DE573742ABF1EB6B CRC64;

-----

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5

Db 453 ADMSW 457

-----

RESULT 11

MRJ5 APIME STANDARD; PRT; 598 AA.

ID MRJ5 APIME STANDARD; PRT; 598 AA.

AC 097432;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Major royal jelly precursor (MRJP-5) (Bee-milk protein).

GN MRJP5.

OSApis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Apida; Apis.

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.

NCBI TaxID=7460;

[1] NCBI TaxID=7460;

RP TISSUE: Head.

RC TISSUE: Head.

RX MEDLINE=9373663; PubMed=10441680;

RA Albert S., Bhattacharya D., Klandiny J., Schmitzova J., Simuth J.;

RT "The family of major royal jelly proteins and its evolution.";

RL J. Mol. Evol. 49:290-297(1999).

-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

HONEYBEE QUEEN.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.

-1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of the nurse honey bee.

-1- SIMILARITY: Belongs to the major royal jelly protein family.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL: AF004842; ABD01205.1; -.

DR InterPro: IPR003534; Royaljelly.

DR Pfam: PF03022; MRJP; 2.

DR PRINTS: PR01366; ROYALJELLY.

KW Signal; Repeat; Glycoprotein.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.

FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 598 AA; 70236 MW; 2C603C7E7ACDF63 CRC64;

-----

Query Match 90.0%; Score 36; DB 1; Length 598;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6

Db 113 DMSWA 117

-----

RESULT 12

PGLR\_PENGR STANDARD; PRT; 376 AA.

ID PGLR\_PENGR STANDARD; PRT; 376 AA.

AC 093853;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Polygalacturonase precursor (EC 3.2.1.15) (Pectinase).

GN PG1.

OS Penicillium griseoeseum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

NCBI TaxID=84562;

[1] NCBI TaxID=84562;

RP SEQUENCE FROM N.A.

RC STRAIN=CCT 6421;

RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;

RT "Cloning and characterization of a gene encoding the endopolygalacturonase of Penicillium griseoeseum.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

-1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.

-1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL: AF085238; AAC83692.1; -.

DR InterPro: IPR000743; Glyco\_hydro\_28.

DR InterPro: IPR006626; PbH1.

DR Pfam: PF00295; Glyco\_hydro\_28; 1.



DR SMART, SM00710; Pdb1; 5.  
 DR PROSITE; PS00502; POLYGLACTURONASE; 1.  
 KM Hydrolase; Glycosidase; Cell wall; Signal.  
 FT SIGNAL 1 20 POTENTIAL  
 FT CHAIN 21 376 POLYGLACTURONASE  
 SQ SEQUENCE 376 AA; 38068 MW; 1EDBEC56ED56928 CRC64;  
 Query Match 85.0%; Score 34; DB 1; Length 376;  
 Best local Similarity 66.7%; Pred. No. 1,1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 Db 349 SDMSWS 354  
 RESULT 13  
 FAS2\_SCHPO STANDARD; PRT; 1842 AA.  
 ID FAS2\_SCHPO 010289; 014163; P78973;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [includes:  
 DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase  
 DE (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier  
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].  
 GN FAS2 OR LSD1 OR SPAC4A8.11C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96354912; PubMed=8769419;  
 RA Saitoh S., Takahashi K., Nabeshima Y., Nakaseko Y.,  
 RA Hirata A., Yanagida M.;  
 RT "Aberrant mitosis in fission yeast mutants defective in fatty acid  
 RT synthetase and acetyl CoA carboxylase.";  
 RL J. Cell Biol. 134:949-961(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21363051; PubMed=11470243;  
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,  
 RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;  
 RT "Very long-chain fatty-acid-containing phospholipids accumulate in  
 RT fatty acid synthase temperature-sensitive mutant strains of the  
 RT fission yeast Schizosaccharomyces pombe fas2/lcd1.";  
 RL Biochim. Biophys. Acta 1532:223-233(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgourou J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grympez B.,  
 RA Welfens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabriel C., Fuchs M., Fitzc. C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Burnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucase M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Amstrong J., Forburg S.L.,  
 RA Cerruti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Snopcewski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 RN [4]  
 RP SEQUENCE OF 1-215 FROM N.A.  
 RA Koken M.H.M., de Rooij J.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE=94245730; PubMed=8186691;  
 RA Kaeslin E., Heyer W.-D.;  
 RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand  
 RT exchange in vitro.";  
 RL J. Biol. Chem. 269:14103-14110(1994).  
 CC -1- FUNCTION: Fatty acid synthase catalyzes the formation of  
 CC long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH.  
 CC The alpha subunit contains domains for: acyl carrier protein,  
 CC 3-oxoacyl-[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-  
 CC carrier-protein] synthase. This subunit coordinates the binding  
 CC of the six beta subunits to the enzyme complex.  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a  
 CC long-chain acyl-CoA + N CoA + N CO(2) + 2N NADP(+) +  
 CC -1- CATALYTIC ACTIVITY: [acyl-[acyl-carrier protein] + malonyl-[acyl-  
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +  
 CC [acyl-carrier protein].  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- SUBUNIT: [alpha(6)beta(6)] hexamers of two multifunctional  
 CC subunits (alpha and beta).  
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM  
 CC OTHER FUNGI.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL, outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, D83412; BA011913.1; -  
 DR EMBL, AB013747; BAB62029.1; -  
 DR EMBL, Z98762; CAB11481.1; -  
 DR EMBL, U82216; AAB39943.1; -  
 DR PIR, A54083; A54083.  
 DR PIR, T38781; T38781.  
 DR PIR, T43409; T43409.  
 DR GenBank, SPAC4A8.11C; -  
 DR InterPro, IPR008278; 4-PPT\_transf.  
 DR InterPro, IPR002582; ACPS.  
 DR InterPro, IPR000794; ketoacyl\_synth.  
 DR InterPro, IPR004568; pantothen\_s.  
 DR InterPro, IPR006162; pantothen\_s.  
 DR Pfam, PF01648; ACPS; 1.  
 DR Pfam, PF00109; ketoacyl\_synth; 1.  
 DR Pfam, PF02801; ketoacyl\_synth\_C; 1.  
 DR ProDom, PD004282; ACPS; 1.  
 DR TrRfam, TRG00556; pantothen; 1.  
 DR PROSITE, PS00012; PHOSPHOPANTHETHEINE; 1.  
 DR PROSITE, PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 KM Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;  
 N Transferrase; NADP; Phosphopantetheine.  
 FT DOMAIN 1 ?  
 FT DOMAIN 2 ?  
 FT BINDING 180 1842 BETA-KETOACYL SYNTHASE.  
 FT ACT SITE 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).  
 FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).  
 FT CONFLICT 107 107 S -> A (IN REF. 4).  
 FT CONFLICT 422 422 K -> R (IN REF. 1).

SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EE571 CRC64;  
Query Match 85.0%; Score 34; DB 1; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 4.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADMSWA 6  
DB 400 SDWNWA 405  
RESULT 14  
NOS3\_SHEEP STANDARD; PRT; 99 AA.  
ID NOS3\_SHEEP  
AC P79209;  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).  
DE NOS3 OR ENOS.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
OC NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TTSUB=Endothelial cells;  
RA Aguan K., Weiner C.P.;  
RT "Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase."  
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases  
CC - FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a GMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).  
CC - CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).  
CC - COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).  
CC - ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).  
CC - SUBUNIT: Homodimer (By similarity).  
CC - SIMILARITY: Belongs to the NOS family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U76738; AAB40705.1; -.  
DR HSSP; P29473; IDOC.  
DR InterPro; IPR004030; NO\_synthase.  
DR Pfam; PF02898; NO\_synthase; 1.  
DR PROSITE; PS60001; NOS; PARTIAL.  
KM Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;  
Query Match 82.5%; Score 33; DB 1; Length 99;  
Best Local Similarity 80.0%; Pred. No. 48;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 65 ADMAW 69  
RESULT 15  
Y132\_METUA STANDARD; PRT; 220 AA.  
ID Y132\_METUA  
AC O57596;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein M70132.  
GN M70132.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.  
OC NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bilt C.V., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake O., Olsen G.J., Fitzgerald L.M., Clayton R.A., Geocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D., Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Huze M.A., Kaine B.P., Bordovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."  
RT Science 273:1058-1073(1996).  
RL Science 273:1058-1073(1996).  
CC - SIMILARITY: TO M JANNASCHII MJ1220 AND MTEC142.  
CC - SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U67470; AAB98113.1; -.  
DR PIR; D64316; D64316.  
DR TIGR; M00132; -.  
DR InterPro; IPR003356; N6\_DNA\_Mtase.  
DR Pfam; PF02384; N6\_Mtase; 1.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 220 AA; 25766 MW; 710DDA84C7A47954 CRC64;  
Query Match 82.5%; Score 33; DB 1; Length 220;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADMSW 5  
DB 33 ADMAW 37  
Search completed: April 26, 2004, 13:07:56  
Job time : 13 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:06:38 ; Search time 23 Seconds  
(without alignments)  
13.468 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSMA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                   | Description       |
|------------|-------|-------------|--------|----|----------------------|-------------------|
| 1          | 37    | 92.5        | 236    | 4  | US-09-632-570-17     | Sequence 17, Appl |
| 2          | 37    | 92.5        | 236    | 4  | US-09-632-575-47     | Sequence 47, Appl |
| 3          | 37    | 92.5        | 938    | 4  | US-09-252-991A-23882 | Sequence 23882, A |
| 4          | 36    | 90.0        | 68     | 4  | US-09-252-991A-18367 | Sequence 18367, A |
| 5          | 36    | 90.0        | 142    | 4  | US-09-252-991A-31533 | Sequence 31533, A |
| 6          | 36    | 90.0        | 174    | 4  | US-09-325-932A-163   | Sequence 163, App |
| 7          | 36    | 90.0        | 225    | 4  | US-09-325-932A-162   | Sequence 162, App |
| 8          | 36    | 90.0        | 242    | 4  | US-09-325-932A-158   | Sequence 3, Appl  |
| 9          | 36    | 90.0        | 378    | 4  | US-09-252-991A-22368 | Sequence 158, App |
| 10         | 36    | 90.0        | 445    | 4  | US-09-252-991A-21704 | Sequence 22368, A |
| 11         | 36    | 90.0        | 462    | 4  | US-08-905-223-274    | Sequence 21704, A |
| 12         | 34    | 85.0        | 74     | 1  | US-08-379-538-2      | Sequence 214, App |
| 13         | 34    | 82.5        | 74     | 1  | US-08-379-538-2      | Sequence 2, Appl  |
| 14         | 33    | 82.5        | 136    | 4  | US-08-774-065-2      | Sequence 2, Appl  |
| 15         | 33    | 82.5        | 164    | 4  | US-09-252-991A-23817 | Sequence 23817, A |
| 16         | 33    | 82.5        | 218    | 1  | US-08-032-848C-10    | Sequence 10, Appl |
| 17         | 33    | 82.5        | 218    | 1  | US-08-438-870-10     | Sequence 10, Appl |
| 18         | 33    | 82.5        | 218    | 2  | US-08-169-948B-34    | Sequence 34, Appl |
| 19         | 33    | 82.5        | 218    | 2  | US-08-448-873-34     | Sequence 34, Appl |
| 20         | 33    | 82.5        | 218    | 3  | US-08-382-452D-34    | Sequence 34, Appl |
| 21         | 33    | 82.5        | 218    | 3  | US-09-216-295-1      | Sequence 1, Appl  |
| 22         | 33    | 82.5        | 218    | 3  | US-08-507-362A-18    | Sequence 18, Appl |
| 23         | 33    | 82.5        | 218    | 4  | US-09-916-494A-34    | Sequence 34, Appl |
| 24         | 33    | 82.5        | 218    | 4  | US-09-632-570-1      | Sequence 1, Appl  |
| 25         | 33    | 82.5        | 218    | 4  | US-09-632-575-31     | Sequence 31, Appl |
| 26         | 33    | 82.5        | 232    | 3  | US-09-146-770-1      | Sequence 1, Appl  |
| 27         | 33    | 82.5        | 232    | 4  | US-09-633-084-1      | Sequence 1, Appl  |

|    |    |      |     |   |                  |                   |
|----|----|------|-----|---|------------------|-------------------|
| 28 | 33 | 82.5 | 232 | 4 | US-10-075-872-1  | Sequence 1, Appl  |
| 29 | 33 | 82.5 | 232 | 4 | US-10-261-997-1  | Sequence 1, Appl  |
| 30 | 33 | 82.5 | 234 | 1 | US-08-032-848C-9 | Sequence 9, Appl  |
| 31 | 33 | 82.5 | 234 | 1 | US-08-438-870-9  | Sequence 9, Appl  |
| 32 | 33 | 82.5 | 234 | 3 | US-09-146-770-3  | Sequence 3, Appl  |
| 33 | 33 | 82.5 | 234 | 3 | US-09-146-770-4  | Sequence 3, Appl  |
| 34 | 33 | 82.5 | 234 | 3 | US-09-216-295-3  | Sequence 3, Appl  |
| 35 | 33 | 82.5 | 234 | 3 | US-09-216-295-4  | Sequence 3, Appl  |
| 36 | 33 | 82.5 | 234 | 4 | US-09-633-084-3  | Sequence 3, Appl  |
| 37 | 33 | 82.5 | 234 | 4 | US-09-633-084-4  | Sequence 3, Appl  |
| 38 | 33 | 82.5 | 234 | 4 | US-10-075-872-3  | Sequence 4, Appl  |
| 39 | 33 | 82.5 | 234 | 4 | US-10-075-872-4  | Sequence 4, Appl  |
| 40 | 33 | 82.5 | 234 | 4 | US-10-261-997-3  | Sequence 3, Appl  |
| 41 | 33 | 82.5 | 234 | 4 | US-10-261-997-4  | Sequence 4, Appl  |
| 42 | 33 | 82.5 | 234 | 4 | US-09-632-570-3  | Sequence 3, Appl  |
| 43 | 33 | 82.5 | 234 | 4 | US-09-632-570-4  | Sequence 4, Appl  |
| 44 | 33 | 82.5 | 234 | 4 | US-09-632-575-33 | Sequence 33, Appl |
| 45 | 33 | 82.5 | 234 | 4 | US-09-632-575-34 | Sequence 34, Appl |

#### ALIGNMENTS

```
RESULT 1
US-09-632-570-17
; Sequence 17, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualletti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-570-17

Query Match 92.5% Score 37; DB 4; Length 236;
Best Local Similarity 83.3% Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ADMSMA 6
Db 63 ADMSMS 68

RESULT 2
US-09-632-575-47
; Sequence 47, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualletti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Tracy M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-575-47
```

Query Match 92.5%; Score 37; DB 4; Length 236;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 63 ADMSWS 68

RESULT 3  
US-09-252-991A-23882  
; Sequence 23882, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23882  
; LENGTH: 938  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23882

Query Match 92.5%; Score 37; DB 4; Length 938;  
Best Local Similarity 83.3%; Pred. No. 3,4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 581 ADMAWA 586

RESULT 4  
US-09-252-991A-18367  
; Sequence 18367, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18367  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6  
Db 2 DMSWA 6

RESULT 5

US-09-252-991A-31533  
; Sequence 31533, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31533  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5  
Db 94 ADMSW 98

RESULT 6  
US-09-325-932A-163  
; Sequence 163, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 163  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Euclalyptus grandis  
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5  
Db 109 ADMSW 113

RESULT 7  
US-09-325-932A-162  
; Sequence 162, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 162  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-162

Query Match  
Best Local Similarity 90.0%; Score 36; DB 4; Length 225;  
Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||||  
DB 100 ADMSW 104

RESULT 8  
US-09-345-236B-3  
Sequence 3, Application US/09345236B  
Patent No. 6521454  
GENERAL INFORMATION:  
APPLICANT: Becnel, James J.  
APPLICANT: Tukuo, Fukuda  
APPLICANT: Moser, Bettina  
APPLICANT: Cockburn, Andrew  
APPLICANT: White, Susan E.  
APPLICANT: Undeen, Albert H.  
TITLE OF INVENTION: No. 6521454e1 Baculoviruses, Insecticidal  
FILE REFERENCE: 21042.0004  
CURRENT FILING DATE: US/09/345,236B  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 242  
TYPE: PRT  
ORGANISM: mosquito baculovirus  
US-09-345-236B-3

Query Match  
Best Local Similarity 90.0%; Score 36; DB 4; Length 242;  
Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||||  
DB 80 DMSWA 84

RESULT 9  
US-09-325-932A-158  
Sequence 158, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:  
APPLICANT: Film, Barry  
APPLICANT: Lasham, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT FILING DATE: US/09/325,932A  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 158  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-158

Query Match  
Best Local Similarity 90.0%; Score 36; DB 4; Length 378;  
Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

|||||  
DB 128 ADMSW 132

RESULT 10  
US-09-252-991A-22368  
Sequence 22368, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22368  
LENGTH: 445  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22368

Query Match  
Best Local Similarity 90.0%; Score 36; DB 4; Length 445;  
Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||||  
DB 304 DMSWA 308

RESULT 11  
US-09-252-991A-21704  
Sequence 21704, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21704  
LENGTH: 462  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21704

Query Match  
Best Local Similarity 90.0%; Score 36; DB 4; Length 462;  
Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||||  
DB 169 DMSWA 173

RESULT 12  
US-08-905-223-274  
Sequence 274, Application US/08905223  
Patent No. 6222029  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste D.  
APPLICANT: Duclercq, Aymeric

APPLICANT: Lacroix, Bruno  
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israel, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 274:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: -26...-1  
IDENTIFICATION METHOD: Von Heijne matrix  
OTHER INFORMATION: score 9.6  
OTHER INFORMATION: seq WLIATLSWSWALC/RI  
US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 19 ASMSWA 24

RESULT 13  
US-08-379-538-2  
Sequence 2, Application US/08379538  
Patent No. 5804554  
GENERAL INFORMATION:  
APPLICANT: Volkman, Robert A.  
APPLICANT: Saccamano, Nicholas A.  
APPLICANT: Nason II, Deane M.  
APPLICANT: Heck, Steven D.  
APPLICANT: Ronau, Robert T.  
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES  
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc  
STREET: 235 East 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,065  
FILING DATE:  
PRIOR APPLICATION NUMBER:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,538  
FILING DATE: 3-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887073  
FILING DATE: 21-MAY-1992  
APPLICATION NUMBER: PCT/US93/03921  
FILING DATE: 30-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Zielinski, Bryan  
REGISTRATION NUMBER: 34,462  
REFERENCE/DOCKET NUMBER: PC8175A  
TELEPHONE: (212) 573-4585  
TELEFAX: (212) 573-1939  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 74 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Filistata hibernalis  
TISSUE TYPE: venom  
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;  
Best Local Similarity 80.0%; Pred. No. 11e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
DB 52 DMSWS 56

RESULT 14  
US-08-774-065-2  
Sequence 2, Application US/08774065  
Patent No. 5989899  
GENERAL INFORMATION:  
APPLICANT: Bower, Benjamin  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Larens, Edmund  
APPLICANT: Ward, Michael  
TITLE OF INVENTION: NOVEL OVERSIZED CELLULOSE COMPOSITIONS  
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENECOR INTERNATIONAL  
STREET: 925 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,065  
FILING DATE:  
PRIOR APPLICATION NUMBER:

FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Glaister, Debra J.  
 REGISTRATION NUMBER: 33,888  
 REFERENCE/DOCKET NUMBER: GC368  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-846-7620  
 TELEFAX: 415-845-6504  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 136 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||:  
 Db 62 ADMQWS 67

RESULT 15  
 US-09-252-991A-23817  
 Sequence 23817, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 PRIOR FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 23817  
 LENGTH: 164  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||:  
 Db 132 AGMSWA 137

Search completed: April 26, 2004, 13:09:56  
 Job time : 24 secs

**This Page Blank (uspto)**

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 26, 2004, 13:07:38 ; Search time 181 Seconds  
(without alignments)  
32.355 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_Main:\*

```
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/2/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/2/paa/US107_COMB.pep.*
33: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
|------------|-------|--------------------|-------|-------------|

|    |    |       |     |                      |                   |
|----|----|-------|-----|----------------------|-------------------|
| 1  | 40 | 100.0 | 6   | US-09-643-260-6      | Sequence 6, Appli |
| 2  | 40 | 100.0 | 6   | US-09-847-946A-41    | Sequence 73, Appl |
| 3  | 40 | 100.0 | 6   | US-09-847-946A-73    | Sequence 41, Appl |
| 4  | 40 | 100.0 | 7   | US-09-847-946A-77    | Sequence 77, Appl |
| 5  | 40 | 100.0 | 8   | US-09-847-946A-78    | Sequence 70, Appl |
| 6  | 40 | 100.0 | 8   | US-09-847-946A-78    | Sequence 78, Appl |
| 7  | 40 | 100.0 | 9   | US-09-847-946A-69    | Sequence 69, Appl |
| 8  | 40 | 100.0 | 9   | US-09-847-946A-72    | Sequence 72, Appl |
| 9  | 40 | 100.0 | 9   | US-09-847-946A-75    | Sequence 75, Appl |
| 10 | 40 | 100.0 | 9   | US-09-847-946A-76    | Sequence 76, Appl |
| 11 | 40 | 100.0 | 10  | US-09-847-946A-71    | Sequence 71, Appl |
| 12 | 40 | 100.0 | 10  | US-09-847-946A-74    | Sequence 74, Appl |
| 13 | 40 | 100.0 | 11  | US-09-847-946A-68    | Sequence 68, Appl |
| 14 | 37 | 92.5  | 33  | PCT-US01-01321-1549  | Sequence 1549, Ap |
| 15 | 37 | 92.5  | 103 | US-09-284-327A-45    | Sequence 45, Appl |
| 16 | 37 | 92.5  | 236 | PCT-US00-33878-47    | Sequence 47, Appl |
| 17 | 37 | 92.5  | 236 | US-09-147-729-16     | Sequence 16, Appl |
| 18 | 37 | 92.5  | 236 | US-09-284-327-22     | Sequence 22, Appl |
| 19 | 37 | 92.5  | 236 | US-09-284-327A-22    | Sequence 22, Appl |
| 20 | 37 | 92.5  | 236 | US-09-470-832-47     | Sequence 47, Appl |
| 21 | 37 | 92.5  | 236 | US-09-632-426-17     | Sequence 17, Appl |
| 22 | 37 | 92.5  | 236 | US-10-441-625-17     | Sequence 17, Appl |
| 23 | 37 | 92.5  | 236 | US-10-441-625-17     | Sequence 17, Appl |
| 24 | 37 | 92.5  | 247 | US-60-142-896-1376   | Sequence 1376, Ap |
| 25 | 37 | 92.5  | 247 | US-60-143-992-1434   | Sequence 1434, Ap |
| 26 | 37 | 92.5  | 597 | US-09-614-150A-14697 | Sequence 14697, A |
| 27 | 37 | 92.5  | 597 | US-09-614-150A-14697 | Sequence 14697, A |
| 28 | 37 | 92.5  | 597 | US-09-791-537-32630  | Sequence 32630, A |
| 29 | 37 | 92.5  | 597 | US-60-173-464-12020  | Sequence 12020, A |
| 30 | 37 | 92.5  | 597 | US-60-191-637-14738  | Sequence 14738, A |
| 31 | 37 | 92.5  | 597 | US-60-191-637-14738  | Sequence 14738, A |
| 32 | 37 | 92.5  | 885 | PCT-US02-03981-5090  | Sequence 5090, Ap |
| 33 | 37 | 92.5  | 885 | US-09-815-242-5090   | Sequence 5090, Ap |
| 34 | 37 | 92.5  | 885 | US-10-072-851-5090   | Sequence 5090, Ap |
| 35 | 37 | 92.5  | 885 | US-10-282-122A-43572 | Sequence 43572, A |
| 36 | 37 | 92.5  | 885 | US-60-253-625-2729   | Sequence 2729, Ap |
| 37 | 37 | 92.5  | 885 | US-60-257-931-3557   | Sequence 3557, Ap |
| 38 | 37 | 92.5  | 885 | US-60-269-308-4579   | Sequence 4579, Ap |
| 39 | 37 | 92.5  | 938 | US-10-366-683-23882  | Sequence 23882, A |
| 40 | 37 | 92.5  | 938 | US-10-418-128-23882  | Sequence 23882, A |
| 41 | 36 | 90.0  | 6   | US-09-643-260-4      | Sequence 4, Appli |
| 42 | 36 | 90.0  | 6   | US-09-643-260-5      | Sequence 5, Appli |
| 43 | 36 | 90.0  | 6   | US-09-847-940B-4     | Sequence 4, Appli |
| 44 | 36 | 90.0  | 6   | US-09-847-940B-4     | Sequence 4, Appli |
| 45 | 36 | 90.0  | 6   | US-09-847-946A-4     | Sequence 4, Appli |

#### ALIGNMENTS

```
US-09-643-260-6
; Sequence 6, Application US/09643260
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: Inhibition of NF-kappa B Activation by Blockade of IKK
; FILE REFERENCE: 44574-5066-US
; CURRENT APPLICATION NUMBER: US/09/643,260
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/201,261
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutant
US-09-643-260-6
```

Query Match 100.0%; Score 40; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 2

US-09-847-946A-41  
; Sequence 41, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 3

US-09-847-946A-73  
; Sequence 73, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence

US-09-847-946A-73  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 4

US-09-847-946A-77  
; Sequence 77, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 77  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 5

US-09-847-946A-70  
; Sequence 70, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence

OTHER INFORMATION: sequence  
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
DB 3 ADMSWA 8

## RESULT 6

US-09-847-946A-78  
Sequence 78, Application US/09847946A

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 78

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-78

Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
DB 1 ADMSWA 6

## RESULT 7

US-09-847-946A-69

Sequence 69, Application US/09847946A

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 69

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
DB 1 ADMSWA 6

## RESULT 8

US-09-847-946A-72

Sequence 72, Application US/09847946A

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 72

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-72

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
DB 1 ADMSWA 6

## RESULT 9

US-09-847-946A-75

Sequence 75, Application US/09847946A

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 75

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
DB 3 ADWSMA 8

## RESULT 10

US-09-847-946A-76  
Sequence 76, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 76  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-76

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
DB 2 ADWSMA 7

## RESULT 11

US-09-847-946A-71  
Sequence 71, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 71  
LENGTH: 10  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-71

Query Match 100.0%; Score 40; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
DB 2 ADWSMA 7

## RESULT 12

US-09-847-946A-74  
Sequence 74, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 74  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-74

Query Match 100.0%; Score 40; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
DB 3 ADWSMA 8

## RESULT 13

US-09-847-946A-68  
Sequence 68, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 11

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-68

Query Match  
Best Local Similarity 100.0%; Score 40; DB 23; Length 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 3 ADWSMA 8

RESULT 14  
PCT-US01-01321-1549  
Sequence 1549, Application PC/TUS0101321  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc., et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC011PCT  
CURRENT APPLICATION NUMBER: PCT/US01/01321  
CURRENT FILING DATE: 2001-01-17  
NUMBER OF SEQ ID NOS: 2181  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 1549  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (3)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US01-01321-1549

Query Match  
Best Local Similarity 92.5%; Score 37; DB 1; Length 33;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 9 ADWTMA 14

RESULT 15  
US-09-284-327A-45  
Sequence 45, Application US/09284327A  
GENERAL INFORMATION:  
APPLICANT: Bower, Benjamin S.  
APPLICANT: Fowler, Timothy  
APPLICANT: Phillips, Jay I.  
TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding  
FILE REFERENCE: GC516-2-US  
CURRENT APPLICATION NUMBER: US/09/284,327A  
CURRENT FILING DATE: 1999-04-10  
PRIOR APPLICATION NUMBER: PCT/US98/26552  
PRIOR FILING DATE: 1998-12-14  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 103  
TYPE: PRT  
ORGANISM: Glaciadium roseum  
US-09-284-327A-45

Query Match  
Best Local Similarity 92.5%; Score 37; DB 16; Length 103;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6

Db 29 ADWSMA 34

Search completed: April 26, 2004, 13:13:10  
Job time: 182 secs

**This Page Blank (uspto)**

---